

**AMENDMENTS TO THE CLAIMS**

1-14. **(Canceled)**

15. **(New)** A method of predicting lymph node metastasis in an individual afflicted with breast cancer, by combining metagene expression data with clinical risk factors, the method comprising:
- (i) obtaining a nucleic sample from a tumor biopsy of the individual and generating an expression profile from the nucleic acid sample of at least two-genes whose expression is correlated with breast cancer recurrence; and
  - (ii) generating a prediction of lymph node metastasis from a classification tree model that incorporates Bayesian analysis for the statistical prediction of binary outcomes, wherein the tree model comprises one or more nodes representing metagenes predictive of lymph node metastasis, and one or more nodes representing clinical risk factors.
16. **(New)** The method of claim 15, wherein the clinical risk factors are selected from auxiliary lymph node status, estrogen receptor (ER) status, tumor size and treatment factors.
17. **(New)** The method of claim 15, wherein one of the metagenes is Mg20.